STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10 560,280
Source: IFW OIPE
Date Processed by STIC: 7/14/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/560,280

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 _✓_ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length — Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/560,280

DATE: 07/14/2006
TIME: 10:27:39

Input Set : **A:\40072-0026US.txt**
Output Set: **N:\CRF4\07142006\J560280.raw**

```
  3 <110> APPLICANT: Takeshi TABIRA
  4        Hideo HARA
  6 <120> TITLE OF INVENTION: A Recombinant Adeno-Associated Virus Vector for
  7        Treatment of Alzheimer Disease
  9 <130> FILE REFERENCE: 40072-0026US
 11 <140> CURRENT APPLICATION NUMBER: US 10/560,280
 12 <141> CURRENT FILING DATE: 2005-12-12
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/008224
 15 <151> PRIOR FILING DATE: 2005-06-11
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-169714
 18 <151> PRIOR FILING DATE: 2003-06-13
 20 <150> PRIOR APPLICATION NUMBER: JP 2003-371103
 21 <151> PRIOR FILING DATE: 2003-10-30
 23 <160> NUMBER OF SEQ ID NOS: 19
 25 <170> SOFTWARE: PatentIn Ver. 2.0
```

Does Not Comply
Corrected Diskette Needed
(pg. 1-3)

ERRORED SEQUENCES

```
       51 <210> SEQ ID NO: 2
       52 <211> LENGTH: 43
       53 <212> TYPE: PRT
       54 <213> ORGANISM: Homo sapiens
       56 <400> SEQUENCE: 2
       57 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
E-->   58 1           5           10          15
       60 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
E-->   61         20          25          30
       63 Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
E-->   64         35          40
       87 <210> SEQ ID NO: 4
       88 <211> LENGTH: 21
       89 <212> TYPE: PRT
       90 <213> ORGANISM: Homo sapiens
       92 <400> SEQUENCE: 4
       93 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
E-->   94 1           5           10          15
       96 Leu Val Phe Phe Ala
E-->   97         20
      118 <210> SEQ ID NO: 6
      119 <211> LENGTH: 18
      120 <212> TYPE: PRT
      121 <213> ORGANISM: Homo sapiens
```

See item #3 on error summary sheet.

RAW SEQUENCE LISTING   DATE: 07/14/2006
PATENT APPLICATION: US/10/560,280   TIME: 10:27:39

Input Set : A:\40072-0026US.txt
Output Set: N:\CRF4\07142006\J560280.raw

```
        123 <400> SEQUENCE: 6
        124 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
E--> 125 1         5              10            15
        127 Ala Leu
        172 <210> SEQ ID NO: 8
        173 <211> LENGTH: 61
        174 <212> TYPE: PRT
        175 <213> ORGANISM: Artificial Sequence
W--> 177 <220> FEATURE:
W--> 177 <223> OTHER INFORMATION:
W--> 177 <400> 8
        178 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
E--> 179 1         5              10            15
        181 Ala Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His
E--> 182      20            25            30
        184 Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala
E--> 185      35            40            45
        187 Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
E--> 188      50            55            60
        231 <210> SEQ ID NO: 10
        232 <211> LENGTH: 39
        233 <212> TYPE: PRT
        234 <213> ORGANISM: Artificial Sequence
W--> 236 <220> FEATURE:
W--> 236 <223> OTHER INFORMATION:
W--> 236 <400> 10
        237 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
E--> 238 1         5              10            15
        240 Ala Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His
E--> 241      20            25            30
        243 Gln Lys Leu Val Phe Phe Ala
E--> 244      35
        348 <210> SEQ ID NO: 19
        349 <211> LENGTH: 18
        350 <212> TYPE: DNA
        351 <213> ORGANISM: Artificial Sequence
        353 <220> FEATURE:
        354 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
        356 <400> SEQUENCE: 19
        357 cggtatcagc tcactcaa                    18
E--> 361 1
```

Same error — pls explain source of genetic material.

?

See error explanation on page 4.

Same error — pls explain

?

Same error

pls delete

<210> 1
<211> 129
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(129)

<400> 1
gat gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa   48
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
 1   5   10   15

ttg gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att   96
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
             20   25   30

gga ctc atg gtg ggc ggt gtt gtc ata gcg aca   129
Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
         35   40

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

(handwritten annotations: "- see item # 3 on = error summary sheet,")

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/14/2006
PATENT APPLICATION: US/10/560,280   TIME: 10:27:40

Input Set : **A:\40072-0026US.txt**
Output Set: **N:\CRF4\07142006\J560280.raw**

Error Explanation:

Use of <220> Feature(NEW RULES):
Sequence(s) __ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:8,10

VERIFICATION SUMMARY   DATE: 07/14/2006
PATENT APPLICATION: **US/10/560,280** TIME: 10:27:40

Input Set : **A:\40072-0026US.txt**
Output Set: **N:\CRF4\07142006\J560280.raw**

```
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:58 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:94 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:125 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:177 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:177 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:177
L:179 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:224 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:236 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:236 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:236 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:236
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:361 M:254 E: No. of Bases conflict, this line has no nucleotides.
```